



#6

# SEQUENCE LISTING

<110> Chern, Maw Shenq  
 Ronald, Pamela  
 The Regents of the University of California

<120> Proteins That Regulate Systemic Acquired Resistance in  
 Plants

<130> 023070-094800US

<140> US 09/294,539

<141> 1999-04-19

<160> 26

<170> PatentIn Ver. 2.1

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<221> CDS

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<223> proline-rich NPR1 interactor (PNI)

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gcc gag aac gcc acc ccg ccc ccg cgc ccg gcg ccc ggc ctc gac ctg	336
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aac gtc gag ccg ccg tcc gac gcg ccg gcc acg ccg cgc tcg gcg cgc	384
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Arg Ser Pro Phe Leu Arg Gly Val Phe Ala Arg Arg Ala Ala Ala Ala	
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His Pro Ala Val Ala Phe Met Ala Gln Val Leu Phe Ala Ala Ser Thr	
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Phe Gln Val Ala Glu Leu Thr Asn Leu Phe Gln Arg Arg Leu Leu Asp	
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Val Leu Asp Lys Val Glu Val Asp Asn Leu Leu Leu Ile Leu Ser Val	
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225 230 235 240	

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Gly Leu Ile Ser Pro Glu Asn Lys Gly Phe Pro Asn Lys His Val Arg	
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Arg Ile His Arg Ala Leu Asp Ser Asp Asp Val Glu Leu Val Arg Met	
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Arg Val Ala Met Asp Ile Ala Gln Val Asp Gly Thr Leu Glu Phe Asn	
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 Val Ser Leu Gly Arg Asp Thr Ser Ala Glu Lys Arg Lys Arg Phe His  
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gac ctg cag gat gtt ctt cag aag gca ttc cac gag gac aag gag gag 1680  
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 Gly Ala Ala Pro Ala Ser Thr Ala Gln Pro Met Leu Tyr Ala Pro Arg  
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 130 135 140

gct acc act tagaagatgt agtgccgtcg cagaaaatta ccagaaaatc 481  
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Leu Val Tyr Val Val Gln Gln Pro Gly Gly Gln Leu Pro Leu Ala Ser  
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Pro Pro Pro Gln Gln Ala Gly His Arg Ser Gly Ser Gly Gly Arg His  
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Gly Gly Ser Gly Ser Arg Tyr Gly Gly Gly Gly Gly Ser Ser Gly Ser  
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 Val Gln Arg Leu Val Ala Arg Asn Asp Ala Val Glu Ala Leu Ser Gly  
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 Gly Gly Glu Ala Ala Ala Gly Leu Gly Ala Gly Met Ala Ala Phe Glu  
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 Ala Ala Arg Gly Ala Pro Ala Pro Arg Ile Gly Val Ala Gln Tyr Leu  
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 gag cgc gtg cac ccg tac gcc ggg ctg gag ccg gag tgc tac gtg gtg 288  
 Glu Arg Val His Arg Tyr Ala Gly Leu Glu Pro Glu Cys Tyr Val Val  
 85 90 95  
 gcg tac gcg tac gtc gac atg gcg gcg cac cgc cgc ccc gcc gcc gcc 336  
 Ala Tyr Ala Tyr Val Asp Met Ala Ala His Arg Arg Pro Ala Ala Ala  
 100 105 110  
 gtc gcc tcc cgc aac gtc cac cgc ctc ctc ctc gcc tgc ctc ctc gtc 384  
 Val Ala Ser Arg Asn Val His Arg Leu Leu Leu Ala Cys Leu Leu Val  
 115 120 125  
 gcc tcc aag gtt ctc gac gac ttc cac cac aac aac gcg ttc ttc gcg 432  
 Ala Ser Lys Val Leu Asp Asp Phe His His Asn Asn Ala Phe Phe Ala  
 130 135 140  
 cgc gtc ggc ggc gtg agc aac gcg gag atg aac agg ctg gag ctg gag 480  
 Arg Val Gly Gly Val Ser Asn Ala Glu Met Asn Arg Leu Glu Leu Glu  
 145 150 155 160

ctc ctc gcc gtg ctg gac ttc gag gtc atg ctc agc cac cgc gtc tac 528  
 Leu Leu Ala Val Leu Asp Phe Glu Val Met Leu Ser His Arg Val Tyr  
 165 170 175  
 gag ctc tac cac gag cac ctc aag aag gag gcg cgg agg gac ggc ggc 576  
 Glu Leu Tyr His Glu His Leu Lys Lys Glu Ala Arg Arg Asp Gly Gly  
 180 185 190  
 gcc ggc gac atg ctc gcc ggc gcg tcg gcc gcc gcc gcc gcc aag gcg 624  
 Ala Gly Asp Met Leu Ala Gly Ala Ser Ala Ala Ala Ala Lys Ala  
 195 200 205  
 ggg aga atg gcg gcc gtc tcg ccg tcc aag ctg ctg gaa cgc gcg gcg 672  
 Gly Arg Met Ala Ala Val Ser Pro Ser Lys Leu Leu Glu Arg Ala Ala  
 210 215 220  
 gtg aac ggc gcc gcg cag cac gac gac tgg agg agc ctg ggt acg gcg 720  
 Val Asn Gly Ala Ala Gln His Asp Asp Trp Arg Ser Leu Gly Thr Ala  
 225 230 235 240  
 gcg gcg gcg gag gcg gcg aac ggc gtg cgg cgg cac agg tcg tcg tcg 768  
 Ala Ala Ala Glu Ala Ala Asn Gly Val Arg Arg His Arg Ser Ser Ser  
 245 250 255  
 tcg tcg cgg tat tcc ttc gat tgc tagtatagcc agcgttgcca aagagcgcgt 822  
 Ser Ser Arg Tyr Ser Phe Asp Cys  
 260  
 tctgtgtgta tatatcaggt tatcaacgag agtttttgag gctgtaaaaa aattaaagac 882  
 ggattaatta cctgccaaag tgccaattag caaatgtttc ccataaaaaa aaaaaaaaaa 942  
 aaaaaaaaaa 951

<210> 10  
 <211> 264  
 <212> PRT  
 <213> Oryza sativa

<400> 10  
 Met Asp Ala Ala Ala Ala Ala Gly Gly Glu Met Ser Arg Gln Lys Ala  
 1 5 10 15  
 Thr Ala Ser Ala Pro Pro Pro Pro Glu Leu Asp Met Val Ala Arg Ala  
 20 25 30  
 Val Gln Arg Leu Val Ala Arg Asn Asp Ala Val Glu Ala Leu Ser Gly  
 35 40 45  
 Gly Gly Glu Ala Ala Ala Gly Leu Gly Ala Gly Met Ala Ala Phe Glu  
 50 55 60  
 Ala Ala Arg Gly Ala Pro Ala Pro Arg Ile Gly Val Ala Gln Tyr Leu  
 65 70 75 80  
 Glu Arg Val His Arg Tyr Ala Gly Leu Glu Pro Glu Cys Tyr Val Val  
 85 90 95  
 Ala Tyr Ala Tyr Val Asp Met Ala Ala His Arg Arg Pro Ala Ala Ala  
 100 105 110

Val Ala Ser Arg Asn Val His Arg Leu Leu Leu Ala Cys Leu Leu Val  
115 120 125

Ala Ser Lys Val Leu Asp Asp Phe His His Asn Asn Ala Phe Phe Ala  
130 135 140

Arg Val Gly Gly Val Ser Asn Ala Glu Met Asn Arg Leu Glu Leu Glu  
145 150 155 160

Leu Leu Ala Val Leu Asp Phe Glu Val Met Leu Ser His Arg Val Tyr  
165 170 175

Glu Leu Tyr His Glu His Leu Lys Lys Glu Ala Arg Arg Asp Gly Gly  
180 185 190

Ala Gly Asp Met Leu Ala Gly Ala Ser Ala Ala Ala Ala Lys Ala  
195 200 205

Gly Arg Met Ala Ala Val Ser Pro Ser Lys Leu Leu Glu Arg Ala Ala  
210 215 220

Val Asn Gly Ala Ala Gln His Asp Asp Trp Arg Ser Leu Gly Thr Ala  
225 230 235 240

Ala Ala Ala Glu Ala Ala Asn Gly Val Arg Arg His Arg Ser Ser Ser  
245 250 255

Ser Ser Arg Tyr Ser Phe Asp Cys  
260

<210> 11  
<211> 621  
<212> DNA  
<213> Oryza sativa

<220>  
<221> CDS  
<222> (1)..(621)  
<223> novel protein that interacts with PNI protein

<400> 11  
agt gct agt gat gaa gcc ctt gca aaa gca gca tct ctg tat gga ggt 48  
Ser Ala Ser Asp Glu Ala Leu Ala Lys Ala Ala Ser Leu Tyr Gly Gly  
1 5 10 15

gct cta aga aat gtt gag aaa gag tac gaa gaa ttt aat aga att tta 96  
Ala Leu Arg Asn Val Glu Lys Glu Tyr Glu Glu Phe Asn Arg Ile Leu  
20 25 30

tct tct cag act ata gat cca ttg agg gct atg gct gca ggc gct ccc 144  
Ser Ser Gln Thr Ile Asp Pro Leu Arg Ala Met Ala Ala Gly Ala Pro  
35 40 45

ctg gaa gat gct cgt ggt ctt gca caa cgt tat agc cgg atg aga cat 192  
Leu Glu Asp Ala Arg Gly Leu Ala Gln Arg Tyr Ser Arg Met Arg His  
50 55 60

gaa gct gag atc ctt tct gct gaa att gct aga agg aag caa cgg gta	240
Glu Ala Glu Ile Leu Ser Ala Glu Ile Ala Arg Arg Lys Gln Arg Val	
65 70 75 80	
cga gaa gct cca gtt gct gag cac act acg aag ctt caa cag tct gaa	288
Arg Glu Ala Pro Val Ala Glu His Thr Thr Lys Leu Gln Gln Ser Glu	
85 90 95	
tct aaa atg ata gag cac aaa gca agc atg gct gtg tta gga aag gaa	336
Ser Lys Met Ile Glu His Lys Ala Ser Met Ala Val Leu Gly Lys Glu	
100 105 110	
gct gct gct gca ctt gcc gct gtt gaa tct cag cag caa agg ata act	384
Ala Ala Ala Ala Leu Ala Ala Val Glu Ser Gln Gln Arg Ile Thr	
115 120 125	
ctt cag cgc ctg gtt ggc atg gta gaa gca gaa aag tta ttt cat ttg	432
Leu Gln Arg Leu Val Gly Met Val Glu Ala Glu Lys Leu Phe His Leu	
130 135 140	
agg tta gct gct ata ctt gat gat gtt gaa gct gag atg tcc tct gaa	480
Arg Leu Ala Ala Ile Leu Asp Asp Val Glu Ala Glu Met Ser Ser Glu	
145 150 155 160	
aag caa aag aga gaa tct gca ccg cct act att cat tct cat aag cgt	528
Lys Gln Lys Arg Glu Ser Ala Pro Pro Thr Ile His Ser His Lys Arg	
165 170 175	
gct gag aag gcc cag tac ttc ctt gct gag gcg gtg cat aac ttc aat	576
Ala Glu Lys Ala Gln Tyr Phe Leu Ala Glu Ala Val His Asn Phe Asn	
180 185 190	
ggt acc aca gaa aag gag ttg agt tta att gtg gtg att atg tcg	621
Gly Thr Thr Glu Lys Glu Leu Ser Leu Ile Val Val Ile Met Ser	
195 200 205	

<210> 12  
 <211> 207  
 <212> PRT  
 <213> Oryza sativa

<400> 12	
Ser Ala Ser Asp Glu Ala Leu Ala Lys Ala Ala Ser Leu Tyr Gly Gly	
1 5 10 15	
Ala Leu Arg Asn Val Glu Lys Glu Tyr Glu Glu Phe Asn Arg Ile Leu	
20 25 30	
Ser Ser Gln Thr Ile Asp Pro Leu Arg Ala Met Ala Ala Gly Ala Pro	
35 40 45	
Leu Glu Asp Ala Arg Gly Leu Ala Gln Arg Tyr Ser Arg Met Arg His	
50 55 60	
Glu Ala Glu Ile Leu Ser Ala Glu Ile Ala Arg Arg Lys Gln Arg Val	
65 70 75 80	
Arg Glu Ala Pro Val Ala Glu His Thr Thr Lys Leu Gln Gln Ser Glu	
85 90 95	

Ser Lys Met Ile Glu His Lys Ala Ser Met Ala Val Leu Gly Lys Glu  
 100 105 110  
 Ala Ala Ala Ala Leu Ala Ala Val Glu Ser Gln Gln Gln Arg Ile Thr  
 115 120 125  
 Leu Gln Arg Leu Val Gly Met Val Glu Ala Glu Lys Leu Phe His Leu  
 130 135 140  
 Arg Leu Ala Ala Ile Leu Asp Asp Val Glu Ala Glu Met Ser Ser Glu  
 145 150 155 160  
 Lys Gln Lys Arg Glu Ser Ala Pro Pro Thr Ile His Ser His Lys Arg  
 165 170 175  
 Ala Glu Lys Ala Gln Tyr Phe Leu Ala Glu Ala Val His Asn Phe Asn  
 180 185 190  
 Gly Thr Thr Glu Lys Glu Leu Ser Leu Ile Val Val Ile Met Ser  
 195 200 205

<210> 13

<211> 444

<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (1)..(441)

<223> GRL1 homologue of glutaredoxin that interacts with  
MN1

<400> 13

atg tac cag gcg atc ccg tac agc agc acc cgg ccg tgg ctc agg ccg 48  
 Met Tyr Gln Ala Ile Pro Tyr Ser Ser Thr Arg Pro Trp Leu Arg Pro  
 1 5 10 15

gag ccg gcg gcg agc gtg gtc gac gtc gtg aag gtg gag acg acg acg 96  
 Glu Pro Ala Ala Ser Val Val Asp Val Val Lys Val Glu Thr Thr Thr  
 20 25 30

gcc gtc gcg ggt cgg ggc ggt gag gcg gag gtc gtg ggg gag gag gag 144  
 Ala Val Ala Gly Arg Gly Gly Glu Ala Glu Val Val Gly Glu Glu Glu  
 35 40 45

gcg gcg gag gtg cgg agg gcg gtg gcg gag agc ccg gtg ctg gtg gtg 192  
 Ala Ala Glu Val Arg Arg Ala Val Ala Glu Ser Pro Val Leu Val Val  
 50 55 60

ggg agg cgc ggg tgc tgc ctc atc cac gtg gtg aag cgg ctg ctg cag 240  
 Gly Arg Arg Gly Cys Cys Leu Ile His Val Val Lys Arg Leu Leu Gln  
 65 70 75 80

ggg ctc ggg gtc aac ccg gcc gtg cac gag gtc gcc ggc gag gcc gcg 288  
 Gly Leu Gly Val Asn Pro Ala Val His Glu Val Ala Gly Glu Ala Ala  
 85 90 95

ctc aag ggg gtt gtg ccg gcc ggt ggg gag gcc gcg gcg ctc ccc gcc 336  
 Leu Lys Gly Val Val Pro Ala Gly Gly Glu Ala Ala Ala Leu Pro Ala  
                   100                                  105                                  110

gtg ttc gtc ggg ggg aag ctc ctc ggc ggg ctc gac cgc ctc atg gcc 384  
 Val Phe Val Gly Gly Lys Leu Leu Gly Gly Leu Asp Arg Leu Met Ala  
                   115                                  120                                  125

gtc cac atc tcc ggc gag ctc gtg ccc atc ctc aag aag gcc ggt gcc 432  
 Val His Ile Ser Gly Glu Leu Val Pro Ile Leu Lys Lys Ala Gly Ala  
                   130                                  135                                  140

ctc tgg ctt taa 444  
 Leu Trp Leu  
 145

<210> 14  
 <211> 147  
 <212> PRT  
 <213> Oryza sativa

<400> 14  
 Met Tyr Gln Ala Ile Pro Tyr Ser Ser Thr Arg Pro Trp Leu Arg Pro  
           1                                  5                                  10                                  15

Glu Pro Ala Ala Ser Val Val Asp Val Val Lys Val Glu Thr Thr Thr  
                   20                                  25                                  30

Ala Val Ala Gly Arg Gly Gly Glu Ala Glu Val Val Gly Glu Glu Glu  
                   35                                  40                                  45

Ala Ala Glu Val Arg Arg Ala Val Ala Glu Ser Pro Val Leu Val Val  
                   50                                  55                                  60

Gly Arg Arg Gly Cys Cys Leu Ile His Val Val Lys Arg Leu Leu Gln  
                   65                                  70                                  75                                  80

Gly Leu Gly Val Asn Pro Ala Val His Glu Val Ala Gly Glu Ala Ala  
                   85                                  90                                  95

Leu Lys Gly Val Val Pro Ala Gly Gly Glu Ala Ala Ala Leu Pro Ala  
                   100                                  105                                  110

Val Phe Val Gly Gly Lys Leu Leu Gly Gly Leu Asp Arg Leu Met Ala  
                   115                                  120                                  125

Val His Ile Ser Gly Glu Leu Val Pro Ile Leu Lys Lys Ala Gly Ala  
                   130                                  135                                  140

Leu Trp Leu  
 145

<210> 15  
 <211> 393  
 <212> DNA  
 <213> Oryza sativa



<220>  
 <221> CDS  
 <222> (1)..(390)  
 <223> GRL2 homologue of glutaredoxin that interacts with  
 MN1

<400> 15  
 atg tac cag gcg atc ccg tac aac gcg aac cgg gct tgg ccg gcg gcg 48  
 Met Tyr Gln Ala Ile Pro Tyr Asn Ala Asn Arg Ala Trp Pro Ala Ala  
 1 5 10 15  
 agc cgg ccg gcg acg gcg ccg ccg ccg ccg ccg ccg ccg cgt gga gag 96  
 Ser Arg Pro Ala Thr Ala Pro Pro Pro Pro Pro Pro Arg Gly Glu  
 20 25 30  
 gag gag gag gtg agg agg gcg gtg gcg gag tgc ccg gtg gtg gtg gtg 144  
 Glu Glu Glu Val Arg Arg Ala Val Ala Glu Cys Pro Val Val Val Val  
 35 40 45  
 ggt cgg agc ggg tgc tgc ctg agc cac gtc gtg aag cgg ctg ctg cag 192  
 Gly Arg Ser Gly Cys Cys Leu Ser His Val Val Lys Arg Leu Leu Gln  
 50 55 60  
 ggg ctc ggg gtc aac ccg gcg gtg cac gag gtc gcc ggc gag gcc gag 240  
 Gly Leu Gly Val Asn Pro Ala Val His Glu Val Ala Gly Glu Ala Glu  
 65 70 75 80  
 ctc gcc ggg gtg gtc gcc ggc ggc ggc ggc gtc gcg ctg ccg gcg gtg 288  
 Leu Ala Gly Val Val Ala Gly Gly Gly Gly Val Ala Leu Pro Ala Val  
 85 90 95  
 ttc gtc ggc ggg agg ctc ctc ggc ggg ctc gac cgg ctc atg gcc gtg 336  
 Phe Val Gly Gly Arg Leu Leu Gly Gly Leu Asp Arg Leu Met Ala Val  
 100 105 110  
 cac atc tcc ggc gag ctc gtg ccc att ctg aag gag gcc ggt gca ctc 384  
 His Ile Ser Gly Glu Leu Val Pro Ile Leu Lys Glu Ala Gly Ala Leu  
 115 120 125  
 tgg ctc tga 393  
 Trp Leu  
 130

<210> 16  
 <211> 130  
 <212> PRT  
 <213> Oryza sativa

<400> 16  
 Met Tyr Gln Ala Ile Pro Tyr Asn Ala Asn Arg Ala Trp Pro Ala Ala  
 1 5 10 15  
 Ser Arg Pro Ala Thr Ala Pro Pro Pro Pro Pro Pro Arg Gly Glu  
 20 25 30  
 Glu Glu Glu Val Arg Arg Ala Val Ala Glu Cys Pro Val Val Val Val  
 35 40 45  
 Gly Arg Ser Gly Cys Cys Leu Ser His Val Val Lys Arg Leu Leu Gln  
 50 55 60

Gly Leu Gly Val Asn Pro Ala Val His Glu Val Ala Gly Glu Ala Glu  
 65 70 75 80  
 Leu Ala Gly Val Val Ala Gly Gly Gly Gly Val Ala Leu Pro Ala Val  
 85 90 95  
 Phe Val Gly Gly Arg Leu Leu Gly Gly Leu Asp Arg Leu Met Ala Val  
 100 105 110  
 His Ile Ser Gly Glu Leu Val Pro Ile Leu Lys Glu Ala Gly Ala Leu  
 115 120 125  
 Trp Leu  
 130

<210> 17  
 <211> 651  
 <212> DNA  
 <213> Oryza sativa

<220>  
 <221> CDS  
 <222> (1)..(651)  
 <223> protein homologue to rat microtubule-associated  
 protein 1A (MAP1A) that interacts with MN1

<400> 17  
 atg ggc tcg tcg gcg gcc gac tcg ttc ccc gcc ggt gga gat gat gca 48  
 Met Gly Ser Ser Ala Ala Asp Ser Phe Pro Ala Gly Gly Asp Asp Ala  
 1 5 10 15  
 atc cga gac gtg tac ggc atc ggt ggt ggt ggg gag gag gac gat ccg 96  
 Ile Arg Asp Val Tyr Gly Ile Gly Gly Gly Gly Glu Glu Asp Asp Pro  
 20 25 30  
 tcc ctc ttc ctc tac ctc tcc gac ctc gcc ccc gtc tcc ccc tcc gcc 144  
 Ser Leu Phe Leu Tyr Leu Ser Asp Leu Ala Pro Val Ser Pro Ser Ala  
 35 40 45  
 tac ctc gac ctc ccc ccc tcg ccg ccg ccg ccg acg acg acg gct acg 192  
 Tyr Leu Asp Leu Pro Pro Ser Pro Pro Pro Pro Thr Thr Thr Ala Thr  
 50 55 60  
 acg atg gtg aag gag ggg gag gag gcg ccg gag gac ctg gtg ctg ccg 240  
 Thr Met Val Lys Glu Gly Glu Glu Ala Pro Glu Asp Leu Val Leu Pro  
 65 70 75 80  
 ttc atc tcg agg atg ctg atc gag gag gac atc gac gac aag ttc ttc 288  
 Phe Ile Ser Arg Met Leu Ile Glu Glu Asp Ile Asp Asp Lys Phe Phe  
 85 90 95  
 tac gac tac ccc gac aac ccg gcg ctg ctc cag gcg cag cag ccc ttc 336  
 Tyr Asp Tyr Pro Asp Asn Pro Ala Leu Leu Gln Ala Gln Gln Pro Phe  
 100 105 110  
 ctc gag atc ctc tcc gat ccc tcc tcc aac tcc cgc tcc tcc aac tcc 384  
 Leu Glu Ile Leu Ser Asp Pro Ser Ser Asn Ser Arg Ser Ser Asn Ser  
 115 120 125

gac gac ccc cgc ctc tcc ccg acc tcc tcc tcc gac acc tcc gcc gcc	432
Asp Asp Pro Arg Leu Ser Pro Thr Ser Ser Ser Asp Thr Ser Ala Ala	
130 135 140	
atc aac tcc tac gac gcc gcc gcc acc gcc acc gcc gtt gcc gcc gcc	480
Ile Asn Ser Tyr Asp Ala Ala Ala Thr Ala Thr Ala Val Ala Ala Ala	
145 150 155 160	
gcg gtg ccc gtg ccg cag tac gag agc atc gag ctc gat ccc gcc gcg	528
Ala Val Pro Val Pro Gln Tyr Glu Ser Ile Glu Leu Asp Pro Ala Ala	
165 170 175	
ttc ttc gcc gcg gcc aac tcc gac ctc atg agc tcc gct tct caa ggg	576
Phe Phe Ala Ala Ala Asn Ser Asp Leu Met Ser Ser Ala Ser Gln Gly	
180 185 190	
gat gga gga ggc gaa caa gtt cct ccc acc gag aac aag ctc gtc atc	624
Asp Gly Gly Gly Glu Gln Val Pro Pro Thr Glu Asn Lys Leu Val Ile	
195 200 205	
gac ctc gag gcc tcg tcg gag aat aat	651
Asp Leu Glu Ala Ser Ser Glu Asn Asn	
210 215	

<210> 18  
 <211> 217  
 <212> PRT  
 <213> Oryza sativa

<400> 18	
Met Gly Ser Ser Ala Ala Asp Ser Phe Pro Ala Gly Gly Asp Asp Ala	
1 5 10 15	
Ile Arg Asp Val Tyr Gly Ile Gly Gly Gly Gly Glu Glu Asp Asp Pro	
20 25 30	
Ser Leu Phe Leu Tyr Leu Ser Asp Leu Ala Pro Val Ser Pro Ser Ala	
35 40 45	
Tyr Leu Asp Leu Pro Pro Ser Pro Pro Pro Thr Thr Thr Ala Thr	
50 55 60	
Thr Met Val Lys Glu Gly Glu Glu Ala Pro Glu Asp Leu Val Leu Pro	
65 70 75 80	
Phe Ile Ser Arg Met Leu Ile Glu Glu Asp Ile Asp Asp Lys Phe Phe	
85 90 95	
Tyr Asp Tyr Pro Asp Asn Pro Ala Leu Leu Gln Ala Gln Gln Pro Phe	
100 105 110	
Leu Glu Ile Leu Ser Asp Pro Ser Ser Asn Ser Arg Ser Ser Asn Ser	
115 120 125	
Asp Asp Pro Arg Leu Ser Pro Thr Ser Ser Ser Asp Thr Ser Ala Ala	
130 135 140	
Ile Asn Ser Tyr Asp Ala Ala Ala Thr Ala Thr Ala Val Ala Ala Ala	
145 150 155 160	

Ala Val Pro Val Pro Gln Tyr Glu Ser Ile Glu Leu Asp Pro Ala Ala  
165 170 175

Phe Phe Ala Ala Ala Asn Ser Asp Leu Met Ser Ser Ala Ser Gln Gly  
180 185 190

Asp Gly Gly Gly Glu Gln Val Pro Pro Thr Glu Asn Lys Leu Val Ile  
195 200 205

Asp Leu Glu Ala Ser Ser Glu Asn Asn  
210 215

<210> 19  
<211> 1005  
<212> DNA  
<213> Oryza sativa

<220>  
<223> rice bZIP protein MN1 cDNA

<220>  
<221> CDS  
<222> (1)..(1002)

<400> 19  
atg gca gat gct agt tca agg act gac aca tcg att gtt gta gac aac 48  
Met Ala Asp Ala Ser Ser Arg Thr Asp Thr Ser Ile Val Val Asp Asn  
1 5 10 15

gac gac aaa aac cac cag tta gaa aac gga cat agt ggt gca gtc atg 96  
Asp Asp Lys Asn His Gln Leu Glu Asn Gly His Ser Gly Ala Val Met  
20 25 30

gct tct aac tct tca gat aga tct gac aga tct gac aaa ctt atg gac 144  
Ala Ser Asn Ser Ser Asp Arg Ser Asp Arg Ser Asp Lys Leu Met Asp  
35 40 45

caa aag aca atg cgg cgg ctt gct caa aat cgt gag gca gca aga aaa 192  
Gln Lys Thr Met Arg Arg Leu Ala Gln Asn Arg Glu Ala Ala Arg Lys  
50 55 60

agt cgg ctg agg aaa aag gca tat gtg caa caa cta gag agc agt aag 240  
Ser Arg Leu Arg Lys Lys Ala Tyr Val Gln Gln Leu Glu Ser Ser Lys  
65 70 75 80

ctg aag ctt gca cag cta gag cag gaa ctt cag aaa gct cgt cag cag 288  
Leu Lys Leu Ala Gln Leu Glu Gln Glu Leu Gln Lys Ala Arg Gln Gln  
85 90 95

gga atc ttc atc tct agc tct gga gac cag acc cat gcc atg agt gga 336  
Gly Ile Phe Ile Ser Ser Ser Gly Asp Gln Thr His Ala Met Ser Gly  
100 105 110

aat ggg gca ttg act ttt gac tta gaa tac act aga tgg ctc gag gag 384  
Asn Gly Ala Leu Thr Phe Asp Leu Glu Tyr Thr Arg Trp Leu Glu Glu  
115 120 125

caa aat aag cag ata aat gag ttg agg aca gca gtg aat gct cat gca	432
Gln Asn Lys Gln Ile Asn Glu Leu Arg Thr Ala Val Asn Ala His Ala	
130 135 140	
agt gac agt gac ctt cgt ctt att gtt gat ggc ata atg gcg cat tat	480
Ser Asp Ser Asp Leu Arg Leu Ile Val Asp Gly Ile Met Ala His Tyr	
145 150 155 160	
gac gag gta ttc aag gtt aag ggt gta gct gca aag gcc gat gtg ttt	528
Asp Glu Val Phe Lys Val Lys Gly Val Ala Ala Lys Ala Asp Val Phe	
165 170 175	
cat ata ctt tca ggc atg tgg aag aca ccc gca gaa aga tgc ttc ctg	576
His Ile Leu Ser Gly Met Trp Lys Thr Pro Ala Glu Arg Cys Phe Leu	
180 185 190	
tgg ctt ggt ggt ttc cgt cca tct gag ctt cta aag ctc cta gca aat	624
Trp Leu Gly Gly Phe Arg Pro Ser Glu Leu Leu Lys Leu Leu Ala Asn	
195 200 205	
cac ctc gaa cct tta acc gag cag cag ttg ctg gga tta aac aac ctc	672
His Leu Glu Pro Leu Thr Glu Gln Gln Leu Leu Gly Leu Asn Asn Leu	
210 215 220	
cag gaa tct tct cag cag gcg gag gat gca ctt tca caa ggt atg gaa	720
Gln Glu Ser Ser Gln Gln Ala Glu Asp Ala Leu Ser Gln Gly Met Glu	
225 230 235 240	
gca ctg cag caa tct ctg gca gat act ttg gct gga tct ctc gct tca	768
Ala Leu Gln Gln Ser Leu Ala Asp Thr Leu Ala Gly Ser Leu Ala Ser	
245 250 255	
tca ggg tct tct ggg aat gtg gcg aac tac atg ggt cag atg gca atg	816
Ser Gly Ser Ser Gly Asn Val Ala Asn Tyr Met Gly Gln Met Ala Met	
260 265 270	
gcc atg ggt aaa cta gga acg ctc gag aat ttc ctt tgc cag gcg gac	864
Ala Met Gly Lys Leu Gly Thr Leu Glu Asn Phe Leu Cys Gln Ala Asp	
275 280 285	
aac ctg cga cag cag aca ttg cat caa atg caa cga att ctg acg atc	912
Asn Leu Arg Gln Gln Thr Leu His Gln Met Gln Arg Ile Leu Thr Ile	
290 295 300	
cgg caa gcc tcg cgt gct ctt ctt gcc ata cac gat tac ttt tca cgc	960
Arg Gln Ala Ser Arg Ala Leu Leu Ala Ile His Asp Tyr Phe Ser Arg	
305 310 315 320	
ttg cgt gct ttg agt tcg ctg tgg ctt gct agg cca cgg gag taa	1005
Leu Arg Ala Leu Ser Ser Leu Trp Leu Ala Arg Pro Arg Glu	
325 330	

<210> 20  
 <211> 334  
 <212> PRT  
 <213> Oryza sativa  
 <223> rice bZIP protein MN1 cDNA

<400> 20

Met Ala Asp Ala Ser Ser Arg Thr Asp Thr Ser Ile Val Val Asp Asn  
1 5 10 15  
Asp Asp Lys Asn His Gln Leu Glu Asn Gly His Ser Gly Ala Val Met  
20 25 30  
Ala Ser Asn Ser Ser Asp Arg Ser Asp Arg Ser Asp Lys Leu Met Asp  
35 40 45  
Gln Lys Thr Met Arg Arg Leu Ala Gln Asn Arg Glu Ala Ala Arg Lys  
50 55 60  
Ser Arg Leu Arg Lys Lys Ala Tyr Val Gln Gln Leu Glu Ser Ser Lys  
65 70 75 80  
Leu Lys Leu Ala Gln Leu Glu Gln Glu Leu Gln Lys Ala Arg Gln Gln  
85 90 95  
Gly Ile Phe Ile Ser Ser Ser Gly Asp Gln Thr His Ala Met Ser Gly  
100 105 110  
Asn Gly Ala Leu Thr Phe Asp Leu Glu Tyr Thr Arg Trp Leu Glu Glu  
115 120 125  
Gln Asn Lys Gln Ile Asn Glu Leu Arg Thr Ala Val Asn Ala His Ala  
130 135 140  
Ser Asp Ser Asp Leu Arg Leu Ile Val Asp Gly Ile Met Ala His Tyr  
145 150 155 160  
Asp Glu Val Phe Lys Val Lys Gly Val Ala Ala Lys Ala Asp Val Phe  
165 170 175  
His Ile Leu Ser Gly Met Trp Lys Thr Pro Ala Glu Arg Cys Phe Leu  
180 185 190  
Trp Leu Gly Gly Phe Arg Pro Ser Glu Leu Leu Lys Leu Leu Ala Asn  
195 200 205  
His Leu Glu Pro Leu Thr Glu Gln Gln Leu Leu Gly Leu Asn Asn Leu  
210 215 220  
Gln Glu Ser Ser Gln Gln Ala Glu Asp Ala Leu Ser Gln Gly Met Glu  
225 230 235 240  
Ala Leu Gln Gln Ser Leu Ala Asp Thr Leu Ala Gly Ser Leu Ala Ser  
245 250 255  
Ser Gly Ser Ser Gly Asn Val Ala Asn Tyr Met Gly Gln Met Ala Met  
260 265 270  
Ala Met Gly Lys Leu Gly Thr Leu Glu Asn Phe Leu Cys Gln Ala Asp  
275 280 285  
Asn Leu Arg Gln Gln Thr Leu His Gln Met Gln Arg Ile Leu Thr Ile  
290 295 300  
Arg Gln Ala Ser Arg Ala Leu Leu Ala Ile His Asp Tyr Phe Ser Arg  
305 310 315 320

Leu Arg Ala Leu Ser Ser Leu Trp Leu Ala Arg Pro Arg Glu  
325 330

<210> 21  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:anchor primer  
SS20

<400> 21  
agggatgttt aataccacta c 21

<210> 22  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:gene-specific  
primer mnl-1

<400> 22  
gaagccatga ctgcacca 18

<210> 23  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:gene-specific  
primer mn8-1

<400> 23  
ttatcgtcgg tatccagga 19

<210> 24  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:anchor primer  
ADR1

<400> 24  
acccgggaga gatcgaattc ggcacga 27

<210> 25  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
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